OIPE

RAW SEQUENCE LISTING   DATE: 10/01/2002
PATENT APPLICATION: US/10/009,445A   TIME: 11:22:36

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 3 <110> APPLICANT: Barclay, Neil A.
 4   Brown, Marion H.
 5   Gorman, Daniel M.
 6   Lanier, Lewis L.
 7   Wright, Gavin J.
 8   Cherwinski, Holly
 9   Phillips, Joseph H.
10   Hoek, Robert M.
11   Sedgwick, Jonathon D.
13 <120> TITLE OF INVENTION: Mammalian Proteins; Related Reagents and Methods
15 <130> FILE REFERENCE: DX01052K1
17 <140> CURRENT APPLICATION NUMBER: 10/009,445A
18 <141> CURRENT FILING DATE: 2002-09-04
20 <150> PRIOR APPLICATION NUMBER: PCT/US00/12998
21 <151> PRIOR FILING DATE: 2000-05-11
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27 <151> PRIOR FILING DATE: 1999-11-03
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51 cac gta gca gta ctc ttg atc tgg ggg gtc ttc gcg gct gag tca agt   162
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55 tgt cct gat aag aat caa aca atg cag aac aat tca tca act atg aca   210
56 Cys Pro Asp Lys Asn Gln Thr Met Gln Asn Asn Ser Ser Thr Met Thr
57 25   30   35   40
59 gaa gtt aac act aca gtg ttt gta cag atg ggt aaa aag gct ctg ctc   258
60 Glu Val Asn Thr Thr Val Phe Val Gln Met Gly Lys Lys Ala Leu Leu
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67 ata acc ctc aga gga cag cct tcc tgc ata ata tcc tac aaa gca gac      354
68 Ile Thr Leu Arg Gly Gln Pro Ser Cys Ile Ile Ser Tyr Lys Ala Asp
69 .            75                  80                  85
71 aca agg gag acc cat gaa agc aac tgc tcg gac aga agc atc acc tgg      402
72 Thr Arg Glu Thr His Glu Ser Asn Cys Ser Asp Arg Ser Ile Thr Trp
73       90                  95                 100
75 gcc tcc aca cct gac ctc gct cct gac ctt cag atc agt gca gtg gcc      450
76 Ala Ser Thr Pro Asp Leu Ala Pro Asp Leu Gln Ile Ser Ala Val Ala
77 105                 110                 115                 120
79 ctc cag cat gaa ggg cgt tac tca tgt gat ata gca gta cct gac ggg      498
80 Leu Gln His Glu Gly Arg Tyr Ser Cys Asp Ile Ala Val Pro Asp Gly
81                     125                 130                 135
83 aat ttc caa aac atc tat gac ctc caa gtg ctg gtg ccc cct gaa gta      546
84 Asn Phe Gln Asn Ile Tyr Asp Leu Gln Val Leu Val Pro Pro Glu Val
85                     140                 145                 150
87 acc cac ttt cca ggg gaa aat aga act gca gtt tgt gag gcg att gca      594
88 Thr His Phe Pro Gly Glu Asn Arg Thr Ala Val Cys Glu Ala Ile Ala
89             155                 160                 165
91 ggc aaa cct gct gcg cag atc tct tgg acg cca gat ggg gat tgt gtc      642
92 Gly Lys Pro Ala Ala Gln Ile Ser Trp Thr Pro Asp Gly Asp Cys Val
93       170                 175                 180
95 gct aag aat gaa tca cac agc aat ggc acc gtg act gtc cgg agc aca      690
96 Ala Lys Asn Glu Ser His Ser Asn Gly Thr Val Thr Val Arg Ser Thr
97 185                 190                 195                 200
99 tgc cac tgg gag cag agc cac gtg tct gtc gtg ttc tgt gtt gtc tct      738
100 Cys His Trp Glu Gln Ser His Val Ser Val Val Phe Cys Val Val Ser
101                     205                 210                 215
103 cac ttg aca act ggt aac cag tct ctg tct ata gaa ctg ggt aga ggg      786
104 His Leu Thr Thr Gly Asn Gln Ser Leu Ser Ile Glu Leu Gly Arg Gly
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116 Cys Arg Lys Cys Lys Leu Pro Lys Ser Gly Ala Thr Pro Asp Ile Glu
117 265                 270                 275                 280
119 gag gat gaa atg cag ccg tat gct agc tac aca gag aag agc aat cca      978
120 Glu Asp Glu Met Gln Pro Tyr Ala Ser Tyr Thr Glu Lys Ser Asn Pro
121                     285                 290                 295
123 ctc tat gat act gtg acc acg acg gag gca cac cca gcg tca caa ggc     1026
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133 ctccaatgga gggaaattag ctcttctgaa gttcttagaa agcacaaatg ttctaatgga   1191
135 tttgccttta agttcttcta tcattggaag tttggaatct ttgctgctac ctgttaattc   1251
137 taggaagaac tgatttaatt attacaaaga aagcacattg ttatggtaaa atatcaaatt   1311
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141 tactaaagca tttcatgtga gttcttccaa aaaagaaaat ccctgtgtat acgacatgat   1431
143 tatggtatgt gtgtgccttt atatgtttgt ttacaaatgt gtatatatgc acacatctga   1491
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169 Gln Met Gly Lys Lys Ala Leu Leu Cys Cys Pro Ser Ile Ser Leu Thr
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173 Lys Val Ile Leu Ile Thr Trp Thr Ile Thr Leu Arg Gly Gln Pro Ser
174 65              70              75              80
177 Cys Ile Ile Ser Tyr Lys Ala Asp Thr Arg Glu Thr His Glu Ser Asn
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181 Cys Ser Asp Arg Ser Ile Thr Trp Ala Ser Thr Pro Asp Leu Ala Pro
182         100             105             110
185 Asp Leu Gln Ile Ser Ala Val Ala Leu Gln His Glu Gly Arg Tyr Ser
186         115             120             125
189 Cys Asp Ile Ala Val Pro Asp Gly Asn Phe Gln Asn Ile Tyr Asp Leu
190     130             135             140
193 Gln Val Leu Val Pro Pro Glu Val Thr His Phe Pro Gly Glu Asn Arg
194 145             150             155             160
197 Thr Ala Val Cys Glu Ala Ile Ala Gly Lys Pro Ala Ala Gln Ile Ser
198             165             170             175
201 Trp Thr Pro Asp Gly Asp Cys Val Ala Lys Asn Glu Ser His Ser Asn
202         180             185             190
205 Gly Thr Val Thr Val Arg Ser Thr Cys His Trp Glu Gln Ser His Val
206     195             200             205
209 Ser Val Val Phe Cys Val Val Ser His Leu Thr Thr Gly Asn Gln Ser
210     210             215             220
213 Leu Ser Ile Glu Leu Gly Arg Gly Gly Asp Gln Leu Leu Gly Ser Tyr
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217 Ile Gln Tyr Ile Ile Pro Ser Ile Ile Ile Leu Ile Ile Ile Gly Cys
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257 aagttgacca gagagggtct caccatgcgc acagttcctt ctgtaccagt gtggaggaaa    180
259 agtactgagt gaagggcaga aaaagagaaa acagaa atg ctc tgc cct tgg aga     234
260                                         Met Leu Cys Pro Trp Arg
261                                         1                   5
263 act gct aac cta ggg cta ctg ttg att ttg act atc ttc tta gtg gcc    282
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265                 10              15              20
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268 Glu Ala Glu Gly Ala Ala Gln Pro Asn Asn Ser Leu Met Leu Gln Thr
269         25              30              35
271 agc aag gag aat cat gct tta gct tca agc agt tta tgt atg gat gaa    378
272 Ser Lys Glu Asn His Ala Leu Ala Ser Ser Ser Leu Cys Met Asp Glu
273     40              45              50
275 aaa cag att aca cag aac tac tcg aaa gta ctc gca gaa gtt aac act    426
276 Lys Gln Ile Thr Gln Asn Tyr Ser Lys Val Leu Ala Glu Val Asn Thr
277 55              60              65                  70
279 tca tgg cct gta aag atg gct aca aat gct gtg ctt tgt tgc cct cct    474
280 Ser Trp Pro Val Lys Met Ala Thr Asn Ala Val Leu Cys Cys Pro Pro
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288 Gly Gln Pro Ser Cys Thr Lys Ala Tyr Lys Lys Glu Thr Asn Glu Thr
289         105             110             115
291 aag gaa acc aac tgt act gat gag aga ata acc tgg gtc tcc aga cct    618
292 Lys Glu Thr Asn Cys Thr Asp Glu Arg Ile Thr Trp Val Ser Arg Pro
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295 gat cag aat tcg gac ctt cag att cgt acc gtg gcc atc act cat gac    666
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301                 155             160             165
303 gga tat cac ctc caa gtg tta gtt aca cct gaa gtg acc ctg ttt caa        762
304 Gly Tyr His Leu Gln Val Leu Val Thr Pro Glu Val Thr Leu Phe Gln
305                 170             175             180
307 aac agg aat aga act gca gta tgc aag gca gtt gca ggg aag cca gct        810
308 Asn Arg Asn Arg Thr Ala Val Cys Lys Ala Val Ala Gly Lys Pro Ala
309         185             190             195
311 gcg cat atc tcc tgg atc cca gag ggc gat tgt gcc act aag caa gaa        858
312 Ala His Ile Ser Trp Ile Pro Glu Gly Asp Cys Ala Thr Lys Gln Glu
313     200             205             210
315 tac tgg agc aat ggc aca gtg act gtt aag agt aca tgc cac tgg gag        906
316 Tyr Trp Ser Asn Gly Thr Val Thr Val Lys Ser Thr Cys His Trp Glu
317 215             220             225             230
319 gtc cac aat gtg tct acc gtg acc tgc cac gtc tcc cat ttg act ggc        954
320 Val His Asn Val Ser Thr Val Thr Cys His Val Ser His Leu Thr Gly
321                 235             240             245
323 aac aag agt ctg tac ata gag cta ctt cct gtt cca ggt gcc aaa aaa        1002
324 Asn Lys Ser Leu Tyr Ile Glu Leu Leu Pro Val Pro Gly Ala Lys Lys
325             250             255             260
327 atc agc aaa att ata tat tcc ata tat cat cct tac tat tat tat tta        1050
328 Ile Ser Lys Ile Ile Tyr Ser Ile Tyr His Pro Tyr Tyr Tyr Tyr Leu
329         265             270             275
331 gac cat cgt ggg att cat ttg gtt gtt gaa agt caa tgg ctg cag aaa        1098
332 Asp His Arg Gly Ile His Leu Val Val Glu Ser Gln Trp Leu Gln Lys
333     280             285             290
335 ata taaattgaat aaaacagaat ctactccagt tgttgaggag gatgaaatgc ..        1151
336 Ile
337 295
339 agccctatgc cagctacaca gagaagaaca atcctctcta tgatactaca aacaaggtga     1211
341 aggcatctga ggcattacaa agtgaagttg acacagacct ccatacttta taagttgttg     1271
343 gactctagta ccaagaaaca acaacaaacg agatacatta taattactgt ctgattttct     1331
345 tacagttcta gaatgaagac ttatattgaa attaggtttt ccaaggttct tagaagacat     1391
347 tttaatggat tctcattcat acccttgtat aattggaatt tttgattctt agctgctacc     1451
349 agctagttct ctgaagaact gatgttatta caaagaaaat acatgcccat gaccaaatat     1511
351 tcaaattgtg caggacagta aataatgaaa accaaatttc ctcaagaaat aactgaagaa     1571
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368             20              25              30
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Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:21;  N Pos.  621,630,633,651,657,660,663,666,669,675,678,693,702,705,708
Seq#:21;  N Pos.  711,714,723,726,732,735,738,747,750,762,765,768,771,774,777
Seq#:21;  N Pos.  780,789,792,798,807,819,822,834,837,843,846,858,861,867,873
Seq#:21;  N Pos.  879,891,900,906,909,912,915,918,939,945,948,954,969,972,981
Seq#:21;  N Pos.  984,993,999,1002,1008,1011,1017,1023,1029,1035,1041,1044
Seq#:24;  N Pos.  9,12,15,18,24,27,30,33,36,39,60,63,66,69,72,78,93,108,111
Seq#:24;  N Pos.  114,117,120,123,129,135,138,144,147,165,168,171,183,186,189
Seq#:24;  N Pos.  192,201,204,207,213,231,237,240,243,249,255,264,276,285,288
Seq#:24;  N Pos.  294,297,300,309,315,318,321,324,333,336,342,351,354,357,360
Seq#:24;  N Pos.  363,375,378,384,396,399,402,408,414,423,432,438,441,444,447
Seq#:24;  N Pos.  450,456,459,468,471,480,483,486,489,498,504,507,513,516,519
Seq#:24;  N Pos.  528,534,537,543,552,555,561,567,573,579,582,585,588,591,594
Seq#:24;  N Pos.  597,600,624,627,630,633,636,642,645,648,654,657,660,669,672
Seq#:24;  N Pos.  675,684,687,693,696,702,705,708,711,714,717,720,723,729,735
Seq#:24;  N Pos.  744,747,750,753,762,765,771,774,780,795,804,807,810
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